BLAST

Basic Local Alignment Search Tool

-

Edit and Resubmit Save Search Strategies Formatting options Download

Protein Sequence (67 letters)

Results for: lcl|15335 None(67aa) ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
    lcl|15335
    lcl|15335
Description
    None
Molecule type
    amino acid
Query Length
    67

Database Name
    nr
Description
    All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental
    samples from WGS projects
Program
    BLASTP 2.2.22+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb
Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro
A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted
substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures]
[Multiple alignment] NEW
                    Search Parameters

Search parameter name Search parameter value

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40

Threshold	11
Composition-based stats	2

Database

Database parameter name Database parameter value

Posted date	Feb 16, 2010 5:41 PM
Number of letters	3,560,334,713
Number of sequences	10,435,126
Entrez query	none

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.315511	0.267
K	0.129695	0.041
H	0.4138	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

|	
Length adjustment	39
Effective length of query	28
Effective length of database	3153364799
Effective search space	88294214372
Effective search space used	88294214372

Graphic Summary
Show Conserved Domains
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

[?] _____

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Color key for alignment scores				
<40	40-50	50-80	80-200	>=200

Query
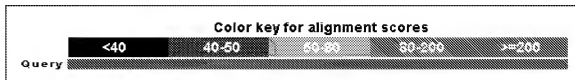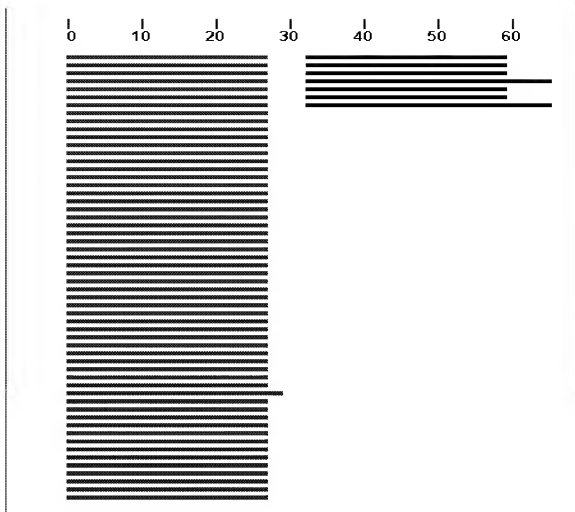
Descriptions

```
                                                                    Score       E
Sequences producing significant alignments:                        (Bits)    Value

gb|AAB25018.1|   PR1(Fv)-PE38KDEL heavy and light chain variabl...   45.1    0.002
gb|AAD09194.1|   anti-asialo GM1 ganglioside antibody heavy cha...   45.1    0.003
pir||A25912   Ig heavy chain precursor V region (W3129) - mouse...   44.7    0.003
sp|P01807.1|HVM37_MOUSE   RecName: Full=Ig heavy chain V region...   44.7    0.003
prf||1005282A   Ig M V-H                                             44.7    0.003
gb|AAH96617.1|   Igh protein [Mus musculus]                          44.7    0.003
sp|P01806.1|HVM36_MOUSE   RecName: Full=Ig heavy chain V region...   44.7    0.003
sp|P01808.1|HVM38_MOUSE   RecName: Full=Ig heavy chain V region...   44.7    0.004
pir||A47329   Ig heavy chain V region (PR1) - mouse                  44.7    0.004
gb|AAA20135.1|   immunoglobulin heavy chain [Mus musculus]           44.3    0.004
gb|AAT06081.1|   immunoglobulin heavy chain variable region [Mu...   44.3    0.004
gb|AAA38079.1|   Ig heavy chain VH-D-JH4 region [Mus musculus]       44.3    0.004
gb|A5O26565.1|   anti-rabies glycoprotein immunoglobulin heavy ...   44.3    0.004
gb|AAO73025.1|   anti-meningococcal polysaccharide group C mono...   44.3    0.004
gb|ABB89741.1|   immunoglobulin heavy chain variable region [Mu...   44.3    0.004
gb|AAQ74725.1|   immunoglobulin mu heavy chain variable region ...   44.3    0.004
prf||1005282D   Ig M V-H                                             44.3    0.004
gb|AAT83547.1|   immunoglobulin gamma 2b heavy chain variable r...   44.3    0.004
gb|AAM12009.1|   monoclonal anti-alpha-1,3-galactosyltransferas...   44.3    0.004
gb|AAQ74712.1|   immunoglobulin mu heavy chain variable region ...   44.3    0.005
gb|AAO19662.1|   immunoglobulin heavy chain variable region [Mu...   44.3    0.005
dbj|BAA74965.1|   natural polyreactive IgA antibody [Mus musculus]   44.3    0.005
gb|AAK68991.1|AF222891_1   monoclonal anti-alpha-1,3-galactosyl...   44.3    0.005
pir||I67528   CD33 antigen homolog - mouse (fragment) >gb|AAP19...   44.3    0.005
gb|AAT81549.1|   immunoglobulin gamma 1 heavy chain variable re...   43.9    0.005
gb|AAO13541.1|   immunoglobulin heavy chain variable region [Mu...   43.9    0.005
gb|AAA38621.1|   Ig heavy chain V-region [Mus musculus]              43.9    0.005
gb|AAC60709.1|   Shigella dysenteriae type 1-specific antibody ...   43.9    0.005
gb|AAQ74729.1|   immunoglobulin mu heavy chain variable region ...   43.9    0.005
gb|AAA38619.1|   Ig heavy chain V-region [Mus musculus]              43.9    0.006
gb|ACI42269.1|   immunoglobulin heavy chain variable region [Mu...   43.9    0.006
gb|ACI42266.1|   immunoglobulin heavy chain variable region [Mu...   43.5    0.007
gb|ACI42252.1|   immunoglobulin heavy chain variable region [Mu...   43.5    0.007
emb|CAA05027.1|   variable region of IgE heavy chain [Mus muscu...   42.7    0.013
pir||S13791   Ig heavy chain V region (X-24) - mouse                 42.4    0.014
prf||1005282C   Ig M V-H                                             42.4    0.014
gb|AAA38620.1|   Ig heavy chain V-region [Mus musculus]              42.4    0.015
pdb|1YUL|H   Chain H, Catalytic Elimination Antibody 34e4 In Co...   42.4    0.015
pdb|3CFJ|H   Chain H, Crystal Structure Of Catalytic Eliminatio...   42.4    0.016
gb|EDL37189.1|   mCG55588 [Mus musculus]                             42.4    0.016
gb|AAA37971.1|   Ig H-chain V-D-region [Mus musculus]                42.4    0.016
sp|P01809.1|HVM39_MOUSE   RecName: Full=Ig heavy chain V region...   42.4    0.016
gb|AAA38338.1|   Ig mu chain V-region [Mus musculus]                 42.4    0.017
gb|AAA38355.1|   immunoglobulin heavy chain VJ region [Mus musc...   42.4    0.018
gb|AAO19012.1|   immunoglobulin heavy chain variable region [Mu...   42.0    0.019
pdb|1UZ8|B   Chain B, Anti-Lewis X Fab Fragment In Complex With...   42.0    0.020
pdb|1UZ6|F   Chain F, Anti-Lewis X Fab Fragment Uncomplexed >pd...   42.0    0.020
emb|CAA25678.1|   unnamed protein product [Mus musculus]             42.0    0.021
pir||I67527   CD33 antigen homolog - mouse (fragment) >gb|AAP20...   42.0    0.022
emb|CAA70114.1|   immunoglobulin heavy chain [Mus musculus]          42.0    0.022
dbj|BAA88633.1|   CN 8 single chain antibody [synthetic construct]   41.2    0.032
prf||1710162B   Ig M L                                               41.2    0.032
```

```
gb|ABD72270.1|   anti-human gastric carcinoma immunoglobulin he...   41.2   0.039
gb|AAK69384.1|AF223151_1   anti-alpha(1,3)Gal monoclonal antibo...   40.8   0.040
gb|AEA42888.1|   anti-CD-38 immunoglobulin heavy chain variable...   40.8   0.047
sp|P01812.1|HVM42_MOUSE   RecName: Full=Ig heavy chain V region...   40.8   0.048
gb|AAC13298.1|   monoclonal antibody aH7:35 IgG1 heavy chain [M...   40.8   0.049
pdb|1Y18|H   Chain H, Fab Fragment Of Catalytic Elimination Ant...   40.8   0.050
dbj|BAC28985.1|   unnamed protein product [Mus musculus]            40.4   0.054
gb|AAA38287.1|   immunoglobulin heavy chain variable region [Mu...   40.4   0.065
gb|AAA91994.1|   immunoglobulin heavy chain [Mus musculus]          40.4   0.065
gb|AAA38290.2|   immunoglobulin active Ab3 heavy chain variable...   40.0   0.069
gb|AAO59819.1|AF458197_1   immunoglobulin heavy chain VDJ [Mus ...   40.0   0.072
sp|P01810.1|HVM40_MOUSE   RecName: Full=Ig heavy chain V region...   40.0   0.079
gb|ACCS9096.1|   anti-sulfadimidine immunoglobulin single chain...   39.7   0.094
pdb|2FBJ|H   Chain H, Refined Crystal Structure Of The Galactan...   39.7   0.10
gb|AAA37953.1|   Ig H-chain V-D-region [Mus musculus]               39.7   0.11
pdb|1OTS|C   Chain C, Structure Of The Escherichia Coli Clc Chl...   39.3   0.12
gb|AAA38080.1|   Ig heavy chain VH-D-JH3 region [Mus musculus]      39.3   0.12
pdb|2H2P|C   Chain C, Crystal Structure Of Clc-Ec1 In Complex W...   39.3   0.12
gb|AAA21376.1|   immunoglobulin heavy chain [Mus musculus]          39.3   0.13
prf||1710162A   Ig M H                                              39.3   0.14
pir||S06817   Ig heavy chain V region (clone 11C7) - mouse >emb...   39.3   0.15
gb|AAA37969.1|   Ig H-chain V-D-region [Mus musculus]               38.9   0.16
gb|AAA38354.1|   immunoglobulin heavy chain VJ region [Mus musc...   38.9   0.17
sp|P01811.1|HVM41_MOUSE   RecName: Full=Ig heavy chain V region...   38.9   0.19
gb|AAA37951.1|   Ig H-chain V-D-region [Mus musculus]               38.5   0.20
gb|AAA38336.1|   Ig mu chain V-region [Mus musculus]                38.1   0.31
gb|AAA37970.1|   Ig H-chain V-D-region [Mus musculus]               38.1   0.32
pdb|2C1O|A   Chain A, Enaiihis Fab Fragment In The Free Form >p...   37.7   0.34
gb|AAA37952.1|   Ig H-chain V-D-region [Mus musculus]               37.7   0.35
gb|AAA38622.1|   Ig heavy chain V-region [Mus musculus]             37.7   0.37
gb|EDL89039.1|   rCG21048 [Rattus norvegicus]                       37.4   0.50
gb|AAA38286.1|   immunoglobulin active Ab3 heavy chain variable...   37.4   0.55
pir||A30560   Ig heavy chain V region (16.4.12E) - mouse (fragm...   37.4   0.55
gb|AAD26785.1|   immunoglobulin heavy chain VH11-JH4 region [Mu...   37.0   0.59
pir||S20709   Ig kappa chain V region - mouse >emb|CAA77975.1|...   37.0   0.70
gb|AAB48807.3|   anti-DNA immunoglobulin light chain IgG [Mus m...   37.0   0.73
emb|CAA84116.1|   monoclonal antibody CB-mab-p24 /13-5 VJ regio...   35.8   1.6
emb|CAB46114.1|   immunoglobulin light chain variable region [M...   35.8   1.6
gb|EDK98812.1|   mCG1036498 [Mus musculus]                          35.4   1.7
gb|AAK68992.1|AF222892_1   monoclonal anti-alpha-1,3-galactosyl...   35.4   1.7
gb|AAA51145.1|   Ig kappa chain [Mus musculus]                      35.4   1.8
gb|EDL83204.1|   rCG64160 [Rattus norvegicus]                       35.4   1.8
gb|AAM16273.1|   immunoglobulin kappa light chain variable regi...   35.4   1.9
pir||S23213   Ig kappa chain precursor V region (BXW14) - mouse...   35.4   2.0
gb|EDK98809.1|   mCG130744 [Mus musculus]                           35.4   2.2
pir||A36259   ig kappa chain V region (TE34) - mouse                35.0   2.2
gb|AAP79429.1|   anti-potato cyst nematode monoclonal antibody ...   35.0   2.6
gb|EDL83206.1|   rCG64161 [Rattus norvegicus]                       34.7   2.9
```

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>gb|AAB25018.1| PR1(Fv)-PE38KDEL heavy and light chain variable region [syntheti
construct]
Length=243

 Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS           EINPDSS INYTPSLKD
Sbjct  27  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  67
```

>gb|AAD09194.1| anti-asialo GM1 ganglioside antibody heavy chain variable region
[Mus musculus]
Length=118

 Score = 45.1 bits (105), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS           EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLESIPEINPDSSTINYTPSLKD  66
```

>pir||A25912 Ig heavy chain precursor V region (W3129) - mouse
 gb|AAA38228.1| Ig H-chain precursor (V-J4-C) [Mus musculus]
Length=139

 Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS           EINPDSS INYTPSLKD
Sbjct  44  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  84
```

>sp|P01807.1|HVM37_MOUSE RecName: Full=Ig heavy chain V region X44
Length=119

 Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS           EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>prf||1005282A Ig M V-H
Length=119

 Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS           EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>gb|AAH96617.1| Igh protein [Mus musculus]
Length=476

 GENE ID: 544903 LOC544903 | similar to immunoglobulin mu-chain [Mus musculus]
(10 or fewer PubMed links)

 Score = 44.7 bits (104), Expect = 0.003, Method: Composition-based stats.
 Identities = 22/41 (53%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF  ++WMS           EINPDSS INY PSLKD
Sbjct  44  GFDFSKDWMSWVRQAPGKGLEWIGEINPDSSTINYAPSLKD  84
```

>sp|P01806.1|HVM36_MOUSE RecName: Full=Ig heavy chain V region 441; Flags: Pre
 emb|CAA24152.1| immunoglobulin heavy chain [Mus musculus]
Length=116

 GENE ID: 195176 Igh-VX24 | immunoglobulin heavy chain (X24 family)
[Mus musculus] (Over 10 PubMed links)

 Score = 44.7 bits (104), Expect = 0.003, Method: Compositional matrix adjust.

```
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS             EINPDSS INYTPSLKD
Sbjct  44  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  84
```

>sp|P01808.1|HVM38_MOUSE RecName: Full=Ig heavy chain V region T601
Length=119

```
 Score = 44.7 bits (104),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS             EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>pir||A47329 Ig heavy chain V region (PR1) - mouse
Length=118

```
 Score = 44.7 bits (104),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS             EINPDSS INYTPSLKD
Sbjct  27  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  67
```

>gb|AAA20135.1| immunoglobulin heavy chain [Mus musculus]
Length=116

```
 Score = 44.3 bits (103),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS             EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>gb|AAT06081.1| immunoglobulin heavy chain variable region [Mus musculus]
Length=122

```
 Score = 44.3 bits (103),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS             EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>gb|AAA38079.1| Ig heavy chain VH-D-JH4 region [Mus musculus]
Length=113

```
 Score = 44.3 bits (103),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS             EINPDSS INYTPSLKD
Sbjct  22  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  62
```

>gb|AB026565.1| anti-rabies glycoprotein immunoglobulin heavy chain variable
region [synthetic construct]
Length=125

```
 Score = 44.3 bits (103),  Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

Query  1   GFDFRRNWMS-------------EINPDSSKINYTPSLKD  27
           GFDF R WMS             EINPDSS INYTPSLKD
Sbjct  25  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  65
```

>gb|AA073025.1| anti-meningococcal polysaccharide group C monoclonal antibody
2010.10 immunoglobulin heavy chain [Mus musculus]

Length=118

 Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS--------------EINPDSSKINYTPSLKD  27
           GFDF R WMS              EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>**gb**|ABB89741.1| immunoglobulin heavy chain variable region [Mus musculus]
Length=115

 Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS--------------EINPDSSKINYTPSLKD  27
           GFDF R WMS              EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>**gb**|AAQ74725.1| immunoglobulin mu heavy chain variable region [Mus musculus]
Length=110

 Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS--------------EINPDSSKINYTPSLKD  27
           GFDF R WMS              EINPDSS INYTPSLKD
Sbjct  18  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  58
```

>**prf**||1005282D Ig M V-H
Length=119

 Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS--------------EINPDSSKINYTPSLKD  27
           GFDF R WMS              EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGPDWIGEINPDSSTINYTPSLKD  66
```

>**gb**|AAT81547.1| immunoglobulin gamma 2b heavy chain variable region [Mus musculu
 gb|AAT81548.1| immunoglobulin gamma 3 heavy chain variable region [Mus musculus
Length=99

 Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS--------------EINPDSSKINYTPSLKD  27
           GFDF R WMS              EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>**gb**|AAM12009.1| monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain
[Mus musculus]
Length=151

 Score = 44.3 bits (103), Expect = 0.004, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS--------------EINPDSSKINYTPSLKD  27
           GFDF R WMS              EINPDSS INYTPSLKD
Sbjct  26  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  66
```

>**gb**|AAQ74712.1| immunoglobulin mu heavy chain variable region [Mus musculus]
Length=104

 Score = 44.3 bits (103), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 24/41 (58%), Positives = 24/41 (58%), Gaps = 14/41 (34%)

```
Query  1   GFDFRRNWMS--------------EINPDSSKINYTPSLKD  27
           GFDF R WMS              EINPDSS INYTPSLKD
Sbjct  18  GFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSLKD  58
```